

AMENDMENTS TO THE SPECIFICATION

Please replace the paragraph on page 45, lines 3-21, with the following:

Capture oligonucleotides of various lengths, including 20, 21, 24, or 26 nucleotides (FV-WT20 (SEQ ID NO: 13): 5'(GGACAGGCGAGGAATACAGG)-(PEG)x3-NH₂, 3' FV-mut21 (SEQ ID NO: 14): 5'(TGGACAGGCAAGGAATACAGG)-(PEG)x3-NH₂ 3', FV-wt24 (SEQ ID NO: 153): 5' TGG ACA GGC GAG GAA TAC AGG TAT-NH₂ 3', FV-mut26 (SEQ ID NO: 164): 5' CTG GAC AGG CAA GGA ATA CAG GTA TT-NH₂ 3') were printed on CodeLink slides as described above and were added to 5 µg of normal human placenta genomic DNA (Sigma, St. Louis, MO) or factor V mutant human genomic DNA (isolated from repository culture GM14899, factor V deficiency, Coriell Institute). The slides and DNA were incubated in 20% FM, 30% FM, or 40% FM, and 4X SSC/0.04% Tween at 40°C for 2 hours in the first step. The slides were then washed in 2XSSC at room temperature for 3 minutes. After washing, nanoparticle probes with detection oligonucleotides that recognized Factor V were added and the mixture was then incubated for 1 hour at 40°C. The signal was detected by silver staining as described above. The results showed that under optimally tuned conditions (30% FM in this case), the human wt DNA generated a signal on the wt probes only, while the human mutant DNA generated a signal only at the mutant capture probes (Figure 8). Changing the stringency conditions resulted in either loss of discrimination (stringency too low) or loss of signal (stringency too high). Figure 9 shows the quantitative data for the perfect (center) hybridization condition in Figure 8.

Please replace the table, on page 49 of the specification and labeled as Table 1, with the following:

Capture	Sequence	TM calculated with HyTher™ (Wayne State University)		
		No corrections	TM correction for hybridization to surface bound probes according to:	
		(35%FM)	Santalucia et al. (35%FM)	Fotin et al. (35%FM)
FII- SNP/Cap1- wt22 (SEQ ID NO: 5)	CTCAGCGAGCCTCAATGCTCCC	46.7	37.0	45.0
FII- SNP/Cap1- mut23 (SEQ ID NO: 6)	CTCTCAGCAAGCCTCAATGCTCC	47.2	35.7	46.3
MTHFR- SNP/Cap6- wt22 (SEQ ID NO: 61)	GATGAAATCGGGCTCCCGCAGAC	40.3	35.5	43.0
MTHFR- SNP/Cap7- mut22 (SEQ ID NO: 2)	ATGAAATCGACTCCCGCAGACA	40.7	36.2	44.0
FV-Cap- WT-24 (SEQ ID NO: +53)	TGGACAGGCGAGGAATACAGGTAT	44.8	35.5	42.9
FV-Cap- mut26 (SEQ ID NO: +64)	CTGGACAGGCAAGGAATACAGGTATT	44.5	35.8	42.9
Probe				
FV-46 (SEQ ID NO: +29)	5' Epi- CCA CAG AAA ATG ATG CCC AGT GCT TAA CAA GAC CAT ACT ACA GTG A 3'	54.8	49.2	57.6
FII-Prol-47 (SEQ ID NO: +07)	5' Epi-TCC TGG AAC CAA TCC CGT GAA AGA ATT ATT TTT GTG TTT CTA AAA CT 3'	52.2	46.9	54.8
MTHFR- Pro II-58 (SEQ ID NO: 8)	5' Epi-AAA GAT CCC GGG GAC GAT GGG GCA AGT GAT GCC CAT GTC GGT GCA TGC CTT CAC AAA G 3'	68.4	58.6	68.5